SEQLIST.TXT

SEQUENCE LISTING

<110> Novartis AG
      McCullough, Karen
      Ide, Susan
      Lavedan, Christian

<120> USE OF GENETIC POLYMORPHISMS THAT
  ASSOCIATE WITH EFFICACY OF TREATMENT OF INFLAMMATORY DISEASE

<130> DV/4-33389A

<150> 60/508,971
<151> 2003-10-06

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<223> TNF locus variant (T at position -1031)

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<223> Tumor necrosis factor alpha (TNFalpha) mRNA
      coding region

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                20                  25                  30

ctc agc ctc ttc tcc ttc ctg atc gtg gca ggc gcc acc acg ctc ttc     144
Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
            35                  40                  45

tgc ctg ctg cac ttt gga gtg atc ggc ccc cag agg gaa gag ttc ccc     192
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
        50                  55                  60

agg gac ctc tct cta atc agc cct ctg gcc cag gca gtc aga tca tct     240
Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65                  70                  75                  80

tct cga acc ccg agt gac aag cct gta gcc cat gtt gta gca aac cct     288
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
                85                  90                  95

caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc     336
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
                100                 105                 110

ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca     384
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
            115                 120                 125

gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc     432
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
        130                 135                 140

tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc     480
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145                 150                 155                 160

gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc     528
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
                165                 170                 175

tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag     576
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
                180                 185                 190

ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc     624
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
            195                 200                 205

agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg     672
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
        210                 215                 220

cag gtc tac ttt ggg atc att gcc ctg tga                             702
Gln Val Tyr Phe Gly Ile Ile Ala Leu  *
225                 230
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         35                  40                  45
Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
     50                  55                  60
Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65                  70                  75                  80
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
                 85                  90                  95
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
             100                 105                 110
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
         115                 120                 125
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
     130                 135                 140
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145                 150                 155                 160
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
                 165                 170                 175
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
             180                 185                 190
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
         195                 200                 205
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
210                 215                 220
Gln Val Tyr Phe Gly Ile Ile Ala Leu
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<210> 9
<211> 1793
<212> DNA
<213> Homo sapiens

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<222> (74)...(1201)
<223> beta-actin expression (ACTB) mRNA coding region

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ccgccagctc acc atg gat gat gat atc gcc gcg ctc gtc gtc gac aac     109
            Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn
            1               5                   10

ggc tcc ggc atg tgc aag gcc ggc ttc gcg ggc gac gat gcc ccc cgg   157
Gly Ser Gly Met Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg
            15                  20                  25

gcc gtc ttc ccc tcc atc gtg ggg cgc ccc agg cac cag ggc gtg atg   205
Ala Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met
        30                  35                  40

gtg ggc atg ggt cag aag gat tcc tat gtg ggc gac gag gcc cag agc   253
Val Gly Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser
45                  50                  55                  60

aag aga ggc atc ctc acc ctg aag tac ccc atc gag cac ggc atc gtc   301
Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val
                65                  70                  75

acc aac tgg gac gac atg gag aaa atc tgg cac cac acc ttc tac aat   349
Thr Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn
            80                  85                  90

gag ctg cgt gtg gct ccc gag gag cac ccc gtg ctg ctg acc gag gcc   397
Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala
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ccc ctg aac ccc aag gcc aac cgc gag aag atg acc cag atc atg ttt      445
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110                     115                     120

gag acc ttc aac acc cca gcc atg tac gtt gct atc cag gct gtg cta      493
Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu
125                     130                     135             140

tcc ctg tac gcc tct ggc cgt acc act ggc atc gtg atg gac tcc ggt      541
Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly
                    145                     150                 155

gac ggg gtc acc cac act gtg ccc atc tac gag ggg tat gcc ctc ccc      589
Asp Gly Val Thr His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro
                160                     165                 170

cat gcc atc ctg cgt ctg gac ctg gct ggc cgg gac ctg act gac tac      637
His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr
                175                     180                 185

ctc atg aag atc ctc acc gag cgc ggc tac agc ttc acc acc acg gcc      685
Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala
                190                     195                 200

gag cgg gaa atc gtg cgt gac att aag gag aag ctg tgc tac gtc gcc      733
Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala
205                     210                     215             220

ctg gac ttc gag caa gag atg gcc acg gct gct tcc agc tcc tcc ctg      781
Leu Asp Phe Glu Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu
                    225                     230                 235

gag aag agc tac gag ctg cct gac ggc cag gtc atc acc att ggc aat      829
Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn
                240                     245                 250

gag cgg ttc cgc tgc cct gag gca ctc ttc cag cct tcc ttc ctg ggc      877
Glu Arg Phe Arg Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly
                255                     260                 265

atg gag tcc tgt ggc atc cac gaa act acc ttc aac tcc atc atg aag      925
Met Glu Ser Cys Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys
270                     275                     280

tgt gac gtg gac atc cgc aaa gac ctg tac gcc aac aca gtg ctg tct      973
Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser
285                     290                     295             300

ggc ggc acc acc atg tac cct ggc att gcc gac agg atg cag aag gag     1021
Gly Gly Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu
                    305                     310                 315

atc act gcc ctg gca ccc agc aca atg aag atc aag atc att gct cct     1069
Ile Thr Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro
                320                     325                 330

cct gag cgc aag tac tcc gtg tgg atc ggc ggc tcc atc ctg gcc tcg     1117
Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser
                335                     340                 345

ctg tcc acc ttc cag cag atg tgg atc agc aag cag gag tat gac gag     1165
Leu Ser Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu
350                     355                     360

tcc ggc ccc tcc atc gtc cac cgc aaa tgc ttc tag gcggactatg         1211
Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe  *
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SEQLIST.TXT

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actcaggatt taaaaactgg aacggtgaag gtgacagcag tcggttggag cgagcatccc 1391
ccaaagttca caatgtggcc gaggactttg attgcacatt gttgtttttt taatagtcat 1451
tccaaatatg agatgcattg ttacaggaag tcccttgcca tcctaaaagc caccccactt 1511
ctctctaagg agaatggccc agtcctctcc caagtccaca caggggaggt gatagcattg 1571
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<222>  (51)...(991)
<223>  chemokine (C C motif) receptor 2 (CCR2) mRNA
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                                                        1


tcc aca tct cgt tct cgg ttt atc aga aat acc aac gag agc ggt gaa   104
Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu
         5                   10                  15


gaa gtc acc acc ttt ttt gat tat gat tac ggt gct ccc tgt cat aaa   152
Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys
     20                  25                  30


ttt gac gtg aag caa att ggg gcc caa ctc ctg cct ccg ctc tac tcg   200
Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser
 35                  40                  45                  50


ctg gtg ttc atc ttt ggt ttt gtg ggc aac atg ctg gtc gtc ctc atc   248
Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile
                 55                  60                  65


tta ata aac tgc aaa aag ctg aag tgc ttg act gac att tac ctg ctc   296
Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu
             70                  75                  80


aac ctg gcc atc tct gat ctg ctt ttt ctt att act ctc cca ttg tgg   344
Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp
             85                  90                  95


gct cac tct gct gca aat gag tgg gtc ttt ggg aat gca atg tgc aaa   392
Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys
        100                 105                 110


tta ttc aca ggg ctg tat cac atc ggt tat ttt ggc gga atc ttc ttc   440
Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe
115                 120                 125                 130


atc atc ctc ctg aca atc gat aga tac ctg gct att gtc cat gct gtg   488
Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val
                135                 140                 145


ttt gct tta aaa gcc agg acg gtc acc ttt ggg gtg gtg aca agt gtg   536
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                150                 155                 160
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act aaa tgc cag aaa gaa gat tct gtt tat gtc tgt ggc cct tat ttt   632
Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe
        180                 185                 190

cca cga gga tgg aat aat ttc cac aca ata atg agg aac att ttg ggg   680
Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly
195                 200                 205                 210

ctg gtc ctg ccg ctg ctc atc atg gtc atc tgc tac tcg gga atc ctg   728
Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu
                215                 220                 225

aaa acc ctg ctt cgg tgt cga aac gag aag aag agg cat agg gca gtg   776
Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val
                230                 235                 240

aga gtc atc ttc acc atc atg att gtt tac ttt ctc ttc tgg act ccc   824
Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro
            245                 250                 255

tat aac att gtc att ctc ctg aac acc ttc cag gaa ttc ttc ggc ctg   872
Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu
        260                 265                 270

agt aac tgt gaa agc acc agt caa ctg gac caa gcc acg cag gtg aca   920
Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr
275                 280                 285                 290

gag act ctt ggg atg act cac tgc tgc atc aat ccc atc atc tat gcc   968
Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala
                295                 300                 305

ttc gtt ggg gag aag ttc aga ag cctttttcac atagctcttg gctgtaggat   1021
Phe Val Gly Glu Lys Phe Arg
                310
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agtgactaca caaggactcc tcgatggtcg tggaaaagga aagtcaattg gcagagcccc 1141
tgaagccagt cttcaggaca aagaaggagc ctagagacag aaatgacaga tctctgcttt 1201
ggaaatcaca cgtctggctt cacagatgtg tgattcacag tgtgaatctt ggtgtctacg 1261
ttaccaggca ggaaggctga gaggagagag actccagctg ggttggaaaa cagtattttc 1321
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tagtaaaaat aaaattaaag ctgaaaactg caacttgtaa atgtggtaaa gagttagttt 1441
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gaagtcatgc gtttaatcac attcgagtgt ttcagtgctt cgcagatgtc cttgatgctc 1801
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tttaaaccct attggtaaag aatggaaggt ggagaagctc cctgaagtaa gcaaagactt 1921
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agagcagaac tttcaccttc atatatttgt atgatcctaa tgaatgcata aaatgttaag 2161
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<213> Homo sapiens

SEQLIST.TXT

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<223> Lymphotoxin alpha (LTA) mRNA coding region

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Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
1               5                   10                  15

cta cac ctc ctc ctt ctg ggg ctg ctg ctg gtt ctg ctg cct ggg gcc    96
Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
            20                  25                  30

cag ggg ctc cct ggt gtt ggc ctc aca cct tca gct gcc cag act gcc   144
Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
        35                  40                  45

cgt cag cac ccc aag atg cat ctt gcc cac agc acc ctc aaa cct gct   192
Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
        50                  55                  60

gct cac ctc att gga gac ccc agc aag cag aac tca ctg ctc tgg aga   240
Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
65                  70                  75                  80

gca aac acg gac cgt gcc ttc ctc cag gat ggt ttc tcc ttg agc aac   288
Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
                85                  90                  95

aat tct ctc ctg gtc ccc acc agt ggc atc tac ttc gtc tac tcc cag   336
Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
            100                 105                 110

gtg gtc ttc tct ggg aaa gcc tac tct ccc aag gcc acc tcc tcc cca   384
Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro
        115                 120                 125

ctc tac ctg gcc cat gag gtc cag ctc ttc tcc tcc cag tac ccc ttc   432
Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
        130                 135                 140

cat gtg cct ctc ctc agc tcc cag aag atg gtg tat cca ggg ctg cag   480
His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
145                 150                 155                 160

gaa ccc tgg ctg cac tcg atg tac cac ggg gct gcg ttc cag ctc acc   528
Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
                165                 170                 175

cag gga gac cag cta tcc acc cac aca gat ggc atc ccc cac cta gtc   576
Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
            180                 185                 190

ctc agc cct agt act gtc ttc ttt gga gcc ttc gct ctg tag           618
Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu *
            195                 200                 205


<210> 12
<211> 894
<212> DNA
<213> Homo sapiens

<220>
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<222> (9)...(743)
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SEQLIST.TXT
<223> Lymphotoxin beta (LTB) mRNA coding region

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         1               5                   10

ggg agg ggt tcc ctc ctg cta gct gtg gca gga gcc act tct ctg gtg   98
Gly Arg Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val
15                  20                  25                  30

acc ttg ttg ctg gcg gtg cct atc act gtc ctg gct gtg ctg gcc tta   146
Thr Leu Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu
                35                  40                  45

gtg ccc cag gat cag gga gga ctg gta acg gag acg gcc gac ccc ggg   194
Val Pro Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly
            50                  55                  60

gca cag gcc cag caa gga ctg ggg ttt cag aag ctg cca gag gag gag   242
Ala Gln Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu
            65                  70                  75

cca gaa aca gat ctc agc ccc ggg ctc cca gct gcc cac ctc ata ggc   290
Pro Glu Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly
        80                  85                  90

gct ccg ctg aag ggg cag ggg cta ggc tgg gag acg acg aag gaa cag   338
Ala Pro Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln
95                  100                 105                 110

gcg ttt ctg acg agc ggg acg cag ttc tcg gac gcc gag ggg ctg gcg   386
Ala Phe Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala
                115                 120                 125

ctc ccg cag gac ggc ctc tat tac ctc tac tgt ctc gtc ggc tac cgg   434
Leu Pro Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg
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Gly Arg Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr
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Leu Arg Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr
160                 165                 170

ccc gag ctg ctg ctc gag ggc gcc gag acg gtg act cca gtg ctg gac   578
Pro Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp
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ccg gcc agg aga caa ggg tac ggg cct ctc tgg tac acg agc gtg ggg   626
Pro Ala Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly
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ttc ggc ggc ctg gtg cag ctc cgg agg ggc gag agg gtg tac gtc aac   674
Phe Gly Gly Leu Val Gln Leu Arg Arg Gly Glu Arg Val Tyr Val Asn
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atc agt cac ccc gat atg gtg gac ttc gcg aga ggg aag acc ttc ttt   722
Ile Ser His Pro Asp Met Val Asp Phe Ala Arg Gly Lys Thr Phe Phe
            225                 230                 235

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Gly Ala Val Met Val Gly *
240

aatattgggg gcccggacgc ccaggacccc atggcagtgg gaaaaatgta ggagactgtt 833
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      Protein 1A (macrophilin 12) mRNA coding region

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Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
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Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
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tat gcc tat ggt gcc act ggg cac cca ggc atc atc cca cca cat gcc   288
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
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